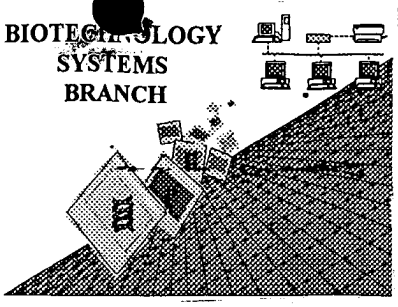
0270

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/686,522

Source: OIPE

Date Processed by STIC: 10/19/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/686,522A

DATE: 06/20/2001
TIME: 14:27:43

Input Set : A:\BB-1165 US NA Corrected Spec.txt
Output Set: N:\CRF3\06202001\I686522A.raw

Does Not Comply
Corrected Diskette Needed

```
      3 <110> APPLICANT: Cahoon, Rebecca E.
      4       Hitz, William D.
      5       Thorpe, Catherine J.
      6       Tingey, Scott V.
      8 <120> TITLE OF INVENTION: PHYTIC ACID BIOSYNTHETIC ENZYMES
     10 <130> FILE REFERENCE: BB1165 US NA
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/686,522A
C--> 13 <141> CURRENT FILING DATE: 2001-06-04
     15 <150> PRIOR APPLICATION NUMBER: 60/082,960
     16 <151> PRIOR FILING DATE: 1998-04-24
     18 <150> PRIOR APPLICATION NUMBER: PCT/US99/08790
     19 <151> PRIOR FILING DATE: 1999-04-22
     21 <160> NUMBER OF SEQ ID NOS: 24
     23 <170> SOFTWARE: Microsoft Office 97
```

ERRORED SEQUENCES

```
    923 <210> SEQ ID NO: 24
    924 <211> LENGTH: 267
    925 <212> TYPE: PRT
    926 <213> ORGANISM: Synechocystis sp.
    928 <400> SEQUENCE: 24
    929 Met Leu Pro Glu Val Glu Gln Arg Leu Phe Ile Ala Gln Gln Leu Ala
    930   1               5                  10                  15
    932 Ala Val Ser Gly Glu Ile Leu Ile Gln Tyr Phe Arg Arg Ser His Leu
    933              20                  25                  30
    935 Gln Gly Gly Thr Lys Ile Asp Gln Val Ser Ala Ile Val Thr Gln Ala
    936          35                  40                  45
    938 Asp Glu Glu Ala Glu Gln Ala Met Val Asp Leu Ile Gln Ala Gln Phe
    939      50                  55                  60
    941 Pro Gln Asp Gly Val Ile Arg Glu Glu Gly Lys Asn Ile Ala Gly Lys
    942  65                  70                  75                  80
    944 Ser Gly Tyr Thr Trp Val Leu Asp Pro Ile Asp Gly Thr Ser Ser Phe
    945                  85                  90                  95
    947 Val Arg Gly Leu Pro Ile Phe Ala Thr Leu Ile Gly Leu Val Asp Ala
    948             100                 105                 110
    950 Asp Met Arg Pro Val Leu Gly Ile Ala His Gln Pro Ile Ser Gly Asp
    951         115                 120                 125
    953 Arg Trp Gln Gly Val Gln Gly Glu Gln Ser Asn Val Asn Gly Ile Pro
    954     130                 135                 140
    956 Leu Val Asn Pro Tyr Lys Ala Ser Glu Ile Asn Leu Thr Ala Ala Cys
    957 145                 150                 155                 160
    959 Ile Val Ser Thr Thr Pro Leu Met Phe Thr Thr Pro Val Gln Gln Gln
    960                 165                 170                 175
    962 Lys Met Ala Asp Ile Tyr Arg Gln Cys Gln Arg Thr Ala Phe Gly Gly
    963             180                 185                 190
```

RAW SEQUENCE LISTING DATE: 06/20/2001
PATENT APPLICATION: US/09/686,522A TIME: 14:27:43

Input Set : A:\BB-1165 US NA Corrected Spec.txt
Output Set: N:\CRF3\06202001\I686522A.raw

```
     965 Asp Cys Phe Asn Tyr Leu Ser Ala Ala Ser Gly Trp Thr Ala Met Pro
     966         195                 200                 205
     968 Leu Val Ile Val Glu Ala Asp Leu Asn Phe Tyr Asp Phe Cys Ala Leu
     969     210                 215                 220
     971 Ile Pro Ile Leu Thr Gly Ala Asn Tyr Cys Phe Thr Asp Trp Gln Gly
     972 225                 230                 235                 240
     974 Lys Glu Leu Thr Pro Glu Ser Thr Glu Val Val Ala Ser Pro Asn Pro
     975                 245                 250                 255
     977 Lys Leu His Ser Glu Ile Leu Ala Phe Leu Gln
     978             260                 265
E--> 982 15
```

VERIFICATION SUMMARY DATE: 06/20/2001
PATENT APPLICATION: US/09/686,522A TIME: 14:27:44

Input Set : A:\BB-1165 US NA Corrected Spec.txt
Output Set: N:\CRF3\06202001\I686522A.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:79 M:283 W: Missing Blank Line separator, <220> field identifier
L:87 M:283 W: Missing Blank Line separator, <220> field identifier
L:91 M:283 W: Missing Blank Line separator, <220> field identifier
L:95 M:283 W: Missing Blank Line separator, <400> field identifier
L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:169 M:283 W: Missing Blank Line separator, <220> field identifier
L:173 M:283 W: Missing Blank Line separator, <400> field identifier
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:430 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:432 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:433 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:982 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:24

OIPE

RAW SEQUENCE LISTING DATE: 10/19/2000
PATENT APPLICATION: US/09/686,522 TIME: 14:53:07

Input Set : A:\BB-1165 US NA Seq Listing.txt
Output Set: N:\CRF3\10192000\I686522.raw

Does Not Comply
Corrected Diskette Needed

see p.3

```
      3 <110> APPLICANT: Cahoon, Rebecca E.
      4       Hitz, William D.
      5       Thorpe, Catherine J.
      6       Tingey, Scott V.
      8 <120> TITLE OF INVENTION: PHYTIC ACID BIOSYNTHETIC ENZYMES
     10 <130> FILE REFERENCE: BB1165 US NA
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/686,522
C--> 13 <141> CURRENT FILING DATE: 2000-10-11
     15 <150> PRIOR APPLICATION NUMBER: 60/082,960
W--> 16 <151> PRIOR FILING DATE: APRIL 24, 1998
     18 <150> PRIOR APPLICATION NUMBER: PCT/US99/08790
W--> 19 <151> PRIOR FILING DATE: APRIL 22, 1999
     21 <160> NUMBER OF SEQ ID NOS: 24
     23 <170> SOFTWARE: Microsoft Office 97
     25 <210> SEQ ID NO: 1
     26 <211> LENGTH: 462
     27 <212> TYPE: DNA
     28 <213> ORGANISM: Oryza sativa
     30 <400> SEQUENCE: 1
     31 cttacatgta agctcgtatt ttcttctcta cacaaccgaa aggtggagcg ttggcgaagg  60
     32 accaaccaat ttcctctctc taatcgccgc ggcgggggat agattgggag tgagcgcgta 120
     33 tggcggagga gcagttcctc gccgtcgcgg tggacgccgc caagaacgcc ggcgagatca 180
     34 tccgcaaggg cttctaccag accaagaacg tggagcacaa gggccaggtg gatttggtga 240
     35 cggagacgga caaggcctgc gaggacctca tcttcaacca cctccggaag cactacccgg 300
     36 accacaagtt catcggcgag gagacgtccg cggggctcgg cgccaccgcg gacctcaccg 360
     37 acgacccgac ctggatcgtc gacccccctcg atggcaccac caatttcgtc catggcttcc 420
     38 cttttgtttg cgtctcgatc ggtctcaccg tcgggaaaat tc                    462
     40 <210> SEQ ID NO: 2
     41 <211> LENGTH: 114
     42 <212> TYPE: PRT
     43 <213> ORGANISM: Oryza sativa
     45 <400> SEQUENCE: 2
     46 Met Ala Glu Glu Gln Phe Leu Ala Val Ala Val Asp Ala Ala Lys Asn
     47   1               5                  10                  15
     49 Ala Gly Glu Ile Ile Arg Lys Gly Phe Tyr Gln Thr Lys Asn Val Glu
     50              20                  25                  30
     52 His Lys Gly Gln Val Asp Leu Val Thr Glu Thr Asp Lys Ala Cys Glu
     53          35                  40                  45
     55 Asp Leu Ile Phe Asn His Leu Arg Lys His Tyr Pro Asp His Lys Phe
     56      50                  55                  60
     58 Ile Gly Glu Glu Thr Ser Ala Gly Leu Gly Ala Thr Ala Asp Leu Thr
     59  65                  70                  75                  80
     61 Asp Asp Pro Thr Trp Ile Val Asp Pro Leu Asp Gly Thr Thr Asn Phe
     62                  85                  90                  95
     64 Val His Gly Phe Pro Phe Val Cys Val Ser Ile Gly Leu Thr Val Gly
     65             100                 105                 110
     67 Lys Ile
```

1998-04-24

1999-04-22

use this date format, per new Sequence Rules

RAW SEQUENCE LISTING DATE: 10/19/2000
PATENT APPLICATION: US/09/686,522 TIME: 14:53:07

Input Set : A:\BB-1165 US NA Seq Listing.txt
Output Set: N:\CRF3\10192000\I686522.raw

68 114
70 <210> SEQ ID NO: 3
71 <211> LENGTH: 561
72 <212> TYPE: DNA
73 <213> ORGANISM: Glycine max
75 <220> FEATURE:
76 <221> NAME/KEY: unsure
77 <222> LOCATION: (529)..(530)
79 <220> FEATURE:
80 <221> NAME/KEY: unsure
81 <222> LOCATION: (543)
83 <220> FEATURE:
84 <221> NAME/KEY: unsure
85 <222> LOCATION: (546)
87 <220> FEATURE:
88 <221> NAME/KEY: unsure
89 <222> LOCATION: (552)
91 <220> FEATURE:
92 <221> NAME/KEY: unsure
93 <222> LOCATION: (556)
95 <400> SEQUENCE: 3
96 gaagaaagca gagcctctac tacatcatca cattcacatt tcagtacctt ctctttctcc 60
97 cagtctctca cacacaacaa ttgaagaaga aaatggttga caatgattcg ctctcggaat 120
98 tcctcgcatc tgcggtcgac gcggctcaga aagctggcga gattattcga aaaggcttct 180
99 accagaccaa aaatgtggaa cacaaaggac aggttgattt ggtcacagaa actgataaag 240
100 catgtgaaga actcatattt aatcatctga aacagcttta tcccactcac aagttcattg 300
101 gggaagagac cacagctgcc tatggcacta cagaacttac agatgaaccc acatggatat 360
102 tgatccctgg atggaactac taacttgtgc atgggttccc tttgtttgtg tcccattggc 420
103 tcacaattgg aaaaatctac aattggtgtt gtatacaatc aatataatga cttttctgga 480
104 tcatggaaaa gtgccttttg atgggaatcc ataaatgtct cacaacgann atcagcctct 540
105 ctncantgag gngganaaaa c 561
107 <210> SEQ ID NO: 4
108 <211> LENGTH: 168
109 <212> TYPE: PRT
110 <213> ORGANISM: Glycine max
112 <400> SEQUENCE: 4
113 Met Val Asp Asn Asp Ser Leu Ser Glu Phe Leu Ala Ser Ala Val Asp
114 1 5 10 15
116 Ala Ala Gln Lys Ala Gly Glu Ile Ile Arg Lys Gly Phe Tyr Gln Thr
117 20 25 30
119 Lys Asn Val Glu His Lys Gly Gln Val Asp Leu Val Thr Glu Thr Asp
120 35 40 45
122 Lys Ala Cys Glu Glu Leu Ile Phe Asn His Leu Lys Gln Leu Tyr Pro
123 50 55 60
125 Thr His Lys Phe Ile Gly Glu Glu Thr Thr Ala Ala Tyr Gly Thr Thr
126 65 70 75 80
128 Glu Leu Thr Asp Glu Pro Thr Trp Ile Val Asp Pro Leu Asp Gly Thr
129 85 90 95
131 Thr Asn Phe Val His Gly Phe Pro Phe Val Cys Val Ser Ile Gly Leu

RAW SEQUENCE LISTING DATE: 10/19/2000
PATENT APPLICATION: US/09/686,522 TIME: 14:53:07

Input Set : A:\BB-1165 US NA Seq Listing.txt
Output Set: N:\CRF3\10192000\I686522.raw

```
132              100                 105                 110
134 Thr Ile Gly Lys Thr Pro Thr Ile Gly Val Val Tyr Asn Pro Ile Ile
135         115                 120                 125
137 Asn Glu Leu Phe Thr Gly Ile His Gly Lys Gly Ala Phe Leu Asn Gly
138     130                 135                 140
140 Asn Pro Ile Lys Val Ser Ser Gln Thr Glu Leu Ile Ser Ser Leu Leu
141 145                 150                 155                 160
143 Ala Thr Glu Ala Gly Thr Lys Arg
144                 165
146 <210> SEQ ID NO: 5
147 <211> LENGTH: 667
148 <212> TYPE: DNA
149 <213> ORGANISM: Glycine max
151 <400> SEQUENCE: 5
152 gaattgcatg tggaaggctg gatgtattct ttgaacttgg ctttggtggt ccttgggatg  60
153 tagcaggtgg tgctgtcatt gttagagaag ctggaggtgt tgtatttgat ccgtccggtg 120
154 cagattttgc aataacatct cagcgagtag cagtttcaaa ccctttctaa aaggatgaac 180
155 ttgtggaaac tcggcgcaaa atggggtggg aaatttacaa ttaaccattg gcaagacctt 240
156 acaagatagc caacctttgt tagtccgtta acctttggcc caaagagttt tttagattcc 300
157 aagttttacg tagaagttcc aggttaaaaa ggttttagaa ttttaacttc ctccgggggc 360
158 tcaagagaat ccataataaa tcaactttaa tccctttaac caagggccaa gtccaacgaa 420
159 aaaaaactcc ctaaacatgg gaagaagcac ctccacaggg cacgcgttcc caaacctggt 480
160 cggaaaggcc gtgggcattc gggaaaccgg taccaatcaa ggatcctccc ggaacccaaa 540
161 ggcaaggcaa accgcggcac gggcttgggc caaaccccgg tgaaccgccg cccaccaacg 600
162 gggagttcaa agcccaaggg gggaaaaggg gactttggcg gtccaaaact ttcacaaccg 660
163 ggggccg                                                         667
165 <210> SEQ ID NO: 6
166 <211> LENGTH: 73
167 <212> TYPE: PRT
168 <213> ORGANISM: Glycine max
170 <400> SEQUENCE: 6
171 Ile Ala Cys Gly Arg Leu Asp Val Phe Phe Glu Leu Gly Phe Gly Gly
172   1               5                  10                  15
174 Pro Trp Asp Val Ala Gly Gly Ala Val Ile Val Arg Glu Ala Gly Gly
175             20                  25                  30
177 Val Val Phe Asp Pro Ser Gly Ala Asp Phe Ala Ile Thr Ser Gln Arg
178         35                  40                  45
W--> 180 Val Ala Val Ser Asn Pro Phe Xaa Lys Asp Glu Leu Val Glu Thr Arg
181     50                  55                  60
183 Arg Lys Met Gly Trp Glu Ile Tyr Asn
184  65                  70
186 <210> SEQ ID NO: 7
187 <211> LENGTH: 1003
188 <212> TYPE: DNA
189 <213> ORGANISM: Triticum aestivum
191 <400> SEQUENCE: 7
192 acgagggaga ttcggaagcc atggcggagg agcagttcct ggccgcagct gtgggcgccg   60
193 ccaagagcgc cggcgagatt atccgcaaga gcttttacct aagcaagaaa gtggagcaca  120
194 agggccaggt ggatttggtg acggagacgg acaaggcatg cgaggatctc atcttcaacc  180
```

see Item 10 on Error Summary Sheet

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

RAW SEQUENCE LISTING DATE: 10/19/2000
PATENT APPLICATION: US/09/686,522 TIME: 14:53:07

Input Set : A:\BB-1165 US NA Seq Listing.txt
Output Set: N:\CRF3\10192000\I686522.raw

```
195 acctccggat gctctacccg gaccacaagt tcatcggcga ggagacgtct gcagccctcg  240
196 gctccaccga tgacctcacc tacgacccca cctggatagt cgacccccctc gatggcacca  300
197 ccaacttcgt tcatggcttt ccttttgtgt gcgtctcgat tggcctcacc attgggaaga  360
198 ttcccaccgt tggagttgtg tacaacccca tcatgaatga gcttttcaca gctgttcgtg  420
199 gaaaaggtgc ttttctcaat ggctctccaa ttaaaacatc gcctcaaaat gagttggtga  480
200 aggctcttat ggtgacagag gtagggacca aaagagacaa gtccactttg gatgatacaa  540
201 ccaacagaat taataagtta ctattcaaga ttagatctat acgtatgtgt ggctctttgg  600
202 ctctaaacat gtgtggagtt gcttgtggta ggctagattt gtgttatgag atcggttttg  660
203 gtggcccctg ggatgtggct gctggagctt tgattctaaa ggaagctggg ggttttgttt  720
204 ttgatccgag cggtgatgag tttgatctga tggcgcaaag aatggcagga tcaaatggcc  780
205 acctcaagga tcagttcatc aaagcattgg gagatgcaag ctgaataact tatttctctt  840
206 ttcaagtaga atgaaagaat gtaagatggc cccaccaata agtaattgag ggctactttt  900
207 tgtgtagttc tatatgcata ttttgcaaac gtggcggatg taatgacatt ggatatattg  960
208 ctcgttttat ttaccatgca aggtgtgatc aaaaaaaaaa aaa                   1003
210 <210> SEQ ID NO: 8
211 <211> LENGTH: 267
212 <212> TYPE: PRT
213 <213> ORGANISM: Triticum aestivum
215 <400> SEQUENCE: 8
216 Met Ala Glu Glu Gln Phe Leu Ala Ala Ala Val Gly Ala Ala Lys Ser
217   1               5                  10                  15
219 Ala Gly Glu Ile Ile Arg Lys Ser Phe Tyr Leu Ser Lys Lys Val Glu
220              20                  25                  30
222 His Lys Gly Gln Val Asp Leu Val Thr Glu Thr Asp Lys Ala Cys Glu
223          35                  40                  45
225 Asp Leu Ile Phe Asn His Leu Arg Met Leu Tyr Pro Asp His Lys Phe
226      50                  55                  60
228 Ile Gly Glu Glu Thr Ser Ala Ala Leu Gly Ser Thr Asp Asp Leu Thr
229  65                  70                  75                  80
231 Tyr Asp Pro Thr Trp Ile Val Asp Pro Leu Asp Gly Thr Thr Asn Phe
232                  85                  90                  95
234 Val His Gly Phe Pro Phe Val Cys Val Ser Ile Gly Leu Thr Ile Gly
235             100                 105                 110
237 Lys Ile Pro Thr Val Gly Val Val Tyr Asn Pro Ile Met Asn Glu Leu
238         115                 120                 125
240 Phe Thr Ala Val Arg Gly Lys Gly Ala Phe Leu Asn Gly Ser Pro Ile
241     130                 135                 140
243 Lys Thr Ser Pro Gln Asn Glu Leu Val Lys Ala Leu Met Val Thr Glu
244 145                 150                 155                 160
246 Val Gly Thr Lys Arg Asp Lys Ser Thr Leu Asp Asp Thr Thr Asn Arg
247                 165                 170                 175
249 Ile Asn Lys Leu Leu Phe Lys Ile Arg Ser Ile Arg Met Cys Gly Ser
250             180                 185                 190
252 Leu Ala Leu Asn Met Cys Gly Val Ala Cys Gly Arg Leu Asp Leu Cys
253         195                 200                 205
255 Tyr Glu Ile Gly Phe Gly Gly Pro Trp Asp Val Ala Ala Gly Ala Leu
256     210                 215                 220
258 Ile Leu Lys Glu Ala Gly Gly Phe Val Phe Asp Pro Ser Gly Asp Glu
259 225                 230                 235                 240
```

RAW SEQUENCE LISTING DATE: 10/19/2000
PATENT APPLICATION: US/09/686,522 TIME: 14:53:07

Input Set : A:\BB-1165 US NA Seq Listing.txt
Output Set: N:\CRF3\10192000\I686522.raw

```
261 Phe Asp Leu Met Ala Gln Arg Met Ala Gly Ser Asn Gly His Leu Lys
262                 245                 250                 255
264 Asp Gln Phe Ile Lys Ala Leu Gly Asp Ala Ser
265             260                 265
267 <210> SEQ ID NO: 9
268 <211> LENGTH: 1090
269 <212> TYPE: DNA
270 <213> ORGANISM: Hordeum vulgare
272 <400> SEQUENCE: 9
273 gcacgaggat aaactgagtg agtcagtcat tcttgaagtc gtgacgaaga acttcagaga   60
274 ccacctcata cttggggagg aaggtggcct tattggagat tctttgtcag agtatctctg  120
275 gtgcattgat cctttagatg gaacaacaaa ctttgcacat ggttacccca gcttttctgt  180
276 atccattggt gttctttatc gaggcaagcc tgctgctgcc actgtggtgg aattttgtgg  240
277 tgggcctatg tgctggagca ctcgtacaat ttctgcatct tctggcaaag gtgcttattg  300
278 taatgggcaa aaaattcatg tcagtccaac agaaaaggtg gaacagtctc ttctggtaac  360
279 tgggtttgga tatgaacatg atgatgcatg gctcaccaat ataaatttgt tcaaggaatt  420
280 tactgatgtt agcaggggag tacgaaggct aggctctgct gctgccgata tgtcccatgt  480
281 tggtctaggc attacagaag cctactggga atatcggctt aagccgtggg acatggctgc  540
282 tggcgttctg atagttgaag aagctggtgg agtagtgaca cgcatggatg gtggggagtt  600
283 tacagtcttt gatcgttctg ttcttgtttc caatggcgtt gttcatgatc agcttttgga  660
284 gcggatccgg cctgctactg aagatcttaa gaagaaagga attgatttct ccttgtggtt  720
285 taagcctgac aagtacccta ccgacttctg aatcacgctg ctcttcagct acttgttctc  780
286 tgtctagcaa aaataaggat gtttttgctg aacaaccatg tacttagact gacaatacat  840
287 ttcaagaccc tttcactcaa ccggatcgaa aattaaagcc gaactttaca taaaggagta  900
288 gagctcgaat gagcttctca ctggattcct tttgctttga tcgaatgtat caggaagaaa  960
289 tgtttgcaaa aggtgttgta tgcatggttc cagcctgttg tacttggaaa aatataactg 1020
290 ccaattttgt caatcatgga taatagcaag atctctcaag aagacatata ctaaaaaaaa 1080
291 aaaaaaaaaa                                                       1090
293 <210> SEQ ID NO: 10
294 <211> LENGTH: 249
295 <212> TYPE: PRT
296 <213> ORGANISM: Hordeum vulgare
298 <400> SEQUENCE: 10
299 His Glu Asp Lys Leu Ser Glu Ser Val Ile Leu Glu Val Val Thr Lys
300   1               5                  10                  15
302 Asn Phe Arg Asp His Leu Ile Leu Gly Glu Glu Gly Gly Leu Ile Gly
303             20                  25                  30
305 Asp Ser Leu Ser Glu Tyr Leu Trp Cys Ile Asp Pro Leu Asp Gly Thr
306         35                  40                  45
308 Thr Asn Phe Ala His Gly Tyr Pro Ser Phe Ser Val Ser Ile Gly Val
309     50                  55                  60
311 Leu Tyr Arg Gly Lys Pro Ala Ala Ala Thr Val Val Glu Phe Cys Gly
312 65                  70                  75                  80
314 Gly Pro Met Cys Trp Ser Thr Arg Thr Ile Ser Ala Ser Ser Gly Lys
315                 85                  90                  95
317 Gly Ala Tyr Cys Asn Gly Gln Lys Ile His Val Ser Pro Thr Glu Lys
318             100                 105                 110
320 Val Glu Gln Ser Leu Leu Val Thr Gly Phe Gly Tyr Glu His Asp Asp
321         115                 120                 125
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VERIFICATION SUMMARY DATE: 10/19/2000
PATENT APPLICATION: US/09/686,522 TIME: 14:53:08

Input Set : A:\BB-1165 US NA Seq Listing.txt
Output Set: N:\CRF3\10192000\I686522.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:16 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:19 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:104 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:104 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
L:105 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
M:340 Repeated in SeqNo=3
L:180 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:180 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:180 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:180 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:180 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:427 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:427 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
L:429 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
M:340 Repeated in SeqNo=13
L:430 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/686,522

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2 ____	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3 ____	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4 ____	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5 ____	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6 ____	Variable Length	Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
7 ____	PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
8 ____	Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: **(2) INFORMATION FOR SEQ ID NO:X:** **(i) SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS") **(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:** **This sequence is intentionally skipped** Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9 ____	Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000
10 ____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
11 ____	Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.
12 ____	Use of <220>Feature (NEW RULES)	Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" **Please explain source of genetic material in <220> to <223> section.** (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
13 ____	PatentIn ver. 2.0 "bug"	**Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.